

Fri Feb 24 15:48:36 2006

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 24, 2006, 15:16:53 ; Search time 567 Seconds  
(without alignments)  
87.743 Million cell updates/sec

Title: CHEN-554-SBQ1

Perfect score: 186

Sequence: 1 VGVAPGVGVAPGVGVAPGVGVAPGVGVAPGVGVAPGV 36

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 7861189 seqs, 1381955077 residues

Total number of hits satisfying chosen parameters: 7861189

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending Patents AA Main:

- 1: /cgn2\_6/ptodata/1/paa/PCTUS COMB pep.\*
- 2: /cgn2\_6/ptodata/1/paa/US066 COMB pep.\*
- 3: /cgn2\_6/ptodata/1/paa/US074 COMB pep.\*
- 4: /cgn2\_6/ptodata/1/paa/US073 COMB pep.\*
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chen-554-seq1.rapm

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- 50: /cgn2\_6/ptodata/1/paa/US606 COMB pep.\*
- 51: /cgn2\_6/ptodata/1/paa/US607 COMB pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Query Match %	Score	Length	DB	ID	Description
1	100.0	186	148	1	PCT-US99-04440-14	Sequence 14, Appl
2	100.0	186	148	22	US-09-258-723-14	Sequence 14, Appl
3	100.0	186	148	28	US-09-841-321A-14	Sequence 14, Appl
4	100.0	186	148	1	PCT-US99-04440-38	Sequence 38, Appl
5	100.0	186	148	22	US-09-258-723-38	Sequence 38, Appl
6	100.0	186	148	28	US-09-841-321A-38	Sequence 38, Appl
7	98.4	183	148	42	US-09-554-996-2	Sequence 2, Appl
8	98.4	183	148	472	US-09-611-523-212	Sequence 212, Appl
9	98.4	183	148	472	US-10-305-278-212	Sequence 212, Appl
10	98.4	183	148	515	US-09-743-818-71	Sequence 71, Appl
11	98.4	183	148	515	US-09-743-818A-71	Sequence 71, Appl
12	98.4	183	148	570	US-10-760-320A-3032	Sequence 3032, Ap
13	98.4	183	148	570	US-10-760-320A-3032	Sequence 3032, Ap
14	98.4	183	148	571	US-09-743-818-7	Sequence 7, Appl
15	98.4	183	148	571	US-09-743-818A-7	Sequence 7, Appl
16	98.4	183	148	617	US-11-072-512-2915	Sequence 2915, Ap
17	98.4	183	148	660	US-09-463-091-5	Sequence 5, Appl
18	98.4	183	148	660	US-09-743-818-6	Sequence 6, Appl
19	98.4	183	148	661	US-09-743-818A-6	Sequence 6, Appl
20	98.4	183	148	692	1 PCT-US02-24483-40	Sequence 40, Appl
21	98.4	183	148	692	US-10-210-172-40	Sequence 40, Appl
22	98.4	183	148	698	US-09-463-091-3	Sequence 3, Appl
23	98.4	183	148	698	US-09-743-818-5	Sequence 5, Appl
24	98.4	183	148	698	US-09-743-818A-5	Sequence 5, Appl
25	98.4	183	148	698	US-11-053-710A-3	Sequence 3, Appl
26	98.4	183	148	702	US-10-170-205E-18017	Sequence 18017, A
27	98.4	183	148	702	US-60-453-050-10290	Sequence 10290, A
28	98.4	183	148	702	US-60-453-135-10290	Sequence 10290, A
29	98.4	183	148	702	US-60-466-412-10290	Sequence 10290, A
30	98.4	183	148	702	US-60-487-610-1797	Sequence 1797, Ap
31	98.4	183	148	702	US-60-582-609-1797	Sequence 1797, Ap
32	98.4	183	148	711	1 PCT-US02-24483-38	Sequence 38, Appl
33	98.4	183	148	711	US-10-210-172-38	Sequence 38, Appl
34	98.4	183	148	712	US-09-554-996-3	Sequence 3, Appl
35	98.4	183	148	730	1 PCT-US03-38193-2566	Sequence 2566, Ap
36	98.4	183	148	730	US-09-554-996-8	Sequence 8, Appl
37	98.4	183	148	730	US-10-723-860-2566	Sequence 2566, Ap
38	98.4	183	148	731	US-09-743-818-4	Sequence 4, Appl
39	98.4	183	148	731	US-09-463-091-2	Sequence 2, Appl
40	98.4	183	148	733	US-09-743-818A-4	Sequence 4, Appl
41	98.4	183	148	733	US-11-053-710A-2	Sequence 2, Appl
42	98.4	183	148	757	1 PCT-US03-09391-2	Sequence 2, Appl
43	98.4	183	148	757	US-09-949-003C-1924	Sequence 29, Appl
44	98.4	183	148	757	PCT-US05-01773-29	Sequence 1924, Ap
45	98.4	183	148	757	US-09-949-003C-1924	Sequence 1924, Ap

# ALIGNMENTS

RESULT 1  
PCT-US99-04440-14  
; Sequence 14, Application PC/TUS9904440  
; GENERAL INFORMATION:  
; APPLICANT: Urry, Dan W.

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: February 18, 2006, 12:15:56 ; Search time 12.2546 Seconds  
(without alignments)  
1432.015 Million cell updates/sec

Title: US-09-554-996-2

Perfect score: 217

Sequence: 1 VGVAPGVGVAPGVGVAPGVG.....PGVGVAPGVGVAPGVGVAPG 42

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA Main:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	217	100.0	617	4	US-10-104-047-2915
2	217	100.0	660	6	US-11-053-710A-5
3	217	100.0	692	4	US-10-210-172-40
4	217	100.0	698	6	US-11-053-710A-3
5	217	100.0	711	4	US-10-210-172-38
6	217	100.0	730	3	US-09-961-403-8
7	217	100.0	733	6	US-10-723-860-2566
8	217	100.0	733	6	US-11-053-710A-2
9	217	100.0	757	5	US-10-287-436A-402
10	217	100.0	757	5	US-10-287-436A-1101
11	217	100.0	757	6	US-11-040-130-29
12	217	100.0	788	5	US-10-852-065-4
13	217	100.0	788	5	US-10-852-065-4
14	214	98.6	148	3	US-09-837-969A-14
15	214	98.6	148	3	US-09-841-321A-14
16	214	98.6	745	3	US-09-837-969A-38
17	214	98.6	745	3	US-09-841-321A-38
18	211	97.2	117	3	US-09-964-662-9
19	211	97.2	118	3	US-09-964-662-10
20	211	97.2	199	3	US-09-964-662-11
21	211	97.2	200	3	US-09-964-662-1
22	211	97.2	731	3	US-09-964-662-1
23	186	85.7	1169	2	US-08-806-029-33
24	181	83.4	119	3	US-09-807-742-15
25	133	61.3	663	4	US-10-108-260A-2477
26	123	56.7	65	4	US-10-117-931-9
27	113	52.1	111	3	US-09-837-969A-13

28	113	52.1	111	3	US-09-837-969A-58	Sequence 58, Appl
29	113	52.1	111	3	US-09-841-321A-13	Sequence 13, Appl
30	113	52.1	111	3	US-09-841-321A-58	Sequence 58, Appl
31	113	52.1	782	3	US-09-837-969A-37	Sequence 37, Appl
32	113	52.1	782	3	US-09-841-321A-37	Sequence 37, Appl
33	113	52.1	832	2	US-08-806-029-27	Sequence 27, Appl
34	113	52.1	936	2	US-08-806-029-26	Sequence 26, Appl
35	113	52.1	972	2	US-08-806-029-30	Sequence 30, Appl
36	113	52.1	988	2	US-08-806-029-28	Sequence 28, Appl
37	113	52.1	1024	2	US-08-806-029-31	Sequence 31, Appl
38	113	52.1	1040	2	US-08-806-029-32	Sequence 32, Appl
39	113	52.1	1056	2	US-08-806-029-29	Sequence 29, Appl
40	113	52.1	2003	3	US-09-837-969A-34	Sequence 34, Appl
41	113	52.1	2003	3	US-09-841-321A-34	Sequence 34, Appl
42	112.5	51.8	40	4	US-10-096-986-43	Sequence 43, Appl
43	112.5	51.8	50	3	US-09-837-969A-29	Sequence 29, Appl
44	112.5	51.8	50	3	US-09-841-321A-29	Sequence 29, Appl
45	112.5	51.8	50	5	US-10-797-606-23	Sequence 23, Appl

## ALIGNMENTS

RESULT 1  
US-10-104-047-2915  
; Sequence 2915, Application US/10104047  
; Publication No. US20030236392A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA  
; FILE REFERENCE: H1-A0105  
; CURRENT APPLICATION NUMBER: US/10/104,047  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER:  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2915  
; LENGTH: 617  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; ORGANISM: Homo sapiens  
US-10-104-047-2915

Query Match 100.0%; Score 217; DB 4; Length 617;  
Best Local Similarity 100.0%; Pred. No. 4.2e-15;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 388 VGVAPGVGVAPGVGVAPGVGLAPGVGVAPGVGVAPGVGVAPG 429

RESULT 2  
US-11-053-710A-5  
; Sequence 5, Application US/11053710A  
; Publication No. US20050204408A1  
; GENERAL INFORMATION:  
; APPLICANT: WEISS, ANTHONY S  
; UNIVERSITY, SYDNEY  
; TITLE OF INVENTION: TROPOLASTIN DERIVATIVES  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GRIFFITH HACK  
; STREET: 168 WALKER STREET  
; CITY: NORTH SYDNEY  
; STATE: NEW SOUTH WALES  
; COUNTRY: AUSTRALIA  
; ZIP: 2060  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC?DOS/MS?DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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2	3652	99.3	730	5	US-10-723-860-2566	Sequence 2566, Ap	
3	3616.5	98.4	711	4	US-10-210-172-38	Sequence 38, Appl	
4	3586.5	97.5	757	5	US-10-287-436A-402	Sequence 402, Appl	
5	3586.5	97.5	757	5	US-10-287-436A-1101	Sequence 1101, Appl	
6	3586.5	97.5	757	6	US-11-040-130-29	Sequence 29, Appl	
7	3561	96.8	788	5	US-10-852-065-4	Sequence 4, Appl	
8	3561	96.8	788	5	US-10-852-575-3	Sequence 3, Appl	
9	3485	94.8	698	6	US-11-053-710A-3	Sequence 3, Appl	
10	3458.5	94.1	731	3	US-09-964-662-1	Sequence 1, Appl	
11	358.5	94.1	733	6	US-11-053-710A-2	Sequence 2, Appl	
12	3416	92.9	692	4	US-10-210-172-40	Sequence 40, Appl	
13	3244.5	88.2	663	4	US-10-108-260A-2477	Sequence 2477, Appl	
14	3118.5	84.8	660	6	US-11-053-710A-5	Sequence 5, Appl	
15	3095.5	84.2	617	4	US-10-104-047-2915	Sequence 2915, Appl	
16	1150	31.3	988	2	US-08-806-029-28	Sequence 28, Appl	
17	1148.5	31.2	965	4	US-10-800-179-31	Sequence 31, Appl	
18	1148.5	31.2	965	5	US-10-845-775A-31	Sequence 31, Appl	
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20	1148.5	31.2	965	5	US-10-939-036-31	Sequence 31, Appl	
21	1136.5	30.9	1038	4	US-10-800-179-30	Sequence 30, Appl	
22	1136.5	30.9	1038	5	US-10-845-775A-30	Sequence 30, Appl	
23	1136.5	30.9	1038	5	US-10-845-936A-30	Sequence 30, Appl	
24	1136.5	30.9	1038	5	US-10-939-036-30	Sequence 30, Appl	
25	1135	30.9	832	2	US-08-806-029-27	Sequence 27, Appl	
26	1133.5	30.8	889	2	US-08-806-029-19	Sequence 19, Appl	
27	1133.5	30.8	936	2	US-08-806-029-26	Sequence 26, Appl	